

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Davis, Roger J.
Flavell, Richard A.
Rakic, Pasko
Whitmarsh, Alan
Kuan, Chia-Yi
Yang, Di
- (ii) TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C.
 - (B) STREET: 225 Franklin Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows 95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/165,522
 - (B) FILING DATE: 02-OCT-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/060,995
 - (B) FILING DATE: 03-OCT-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fasse, J. Peter
 - (B) REGISTRATION NUMBER: 32,983
 - (C) REFERENCE/DOCKET NUMBER: 10363/005001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617/542-5070
 - (B) TELEFAX: 617/542-8906
 - (C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 68...1459

JUN 09 2000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TECH CENTER

TTATGCAAGA AACTGTTGAA TTAGACCCGT TTCCTATAGA TGAGAAACCA TACAAGCTGT	60
GGTATTT ATG AGC CTC CAT TTC TTA TAC TAC TGC AGT GAA CCA ACA TTG	109
Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu	
1 5 10	
GAT GTG AAA ATT GCC TTT TGT CAG GGA TTC GAT AAA CAA GTG GAT GTG	157
Asp Val Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val	
15 20 25 30	
TCA TAT ATT GCC AAA CAT TAC AAC ATG AGC AAA AGC AAA GTT GAC AAC	205
Ser Tyr Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn	
35 40 45	
CAG TTC TAC AGT GTG GAA GTG GGA GAC TCA ACC TTC ACA GTT CTC AAG	253
Gln Phe Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys	
50 55 60	
CGC TAC CAG AAT CTA AAG CCT ATT GGC TCT GGG GCT CAG GGC ATA GTT	301
Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val	
65 70 75	
TGT GCC GCG TAT GAT GCT GTC CTT GAC AGA AAT GTG GCC ATT AAG AAG	349
Cys Ala Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys	
80 85 90	
CTC AGC AGA CCC TTT CAG AAC CAA ACA CAT GCC AAG AGA GCG TAC CGG	397
Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg	
95 100 105 110	
GAG CTG GTC CTC ATG AAG TGT GTG AAC CAT AAA AAC ATT ATT AGT TTA	445
Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu	
115 120 125	
TTA AAT GTC TTC ACA CCC CAG AAA ACG CTG GAG GAG TTC CAA GAT GTT	493
Leu Asn Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val	
130 135 140	
TAC TTA GTA ATG GAA CTG ATG GAT GCC AAC TTA TGT CAA GTG ATT CAG	541
Tyr Leu Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile Gln	
145 150 155	
ATG GAA TTA GAC CAT GAG CGA ATG TCT TAC CTG CTG TAC CAA ATG TTG	589
Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu	
160 165 170	
TGT GGC ATT AAG CAC CTC CAT TCT GCT GGA ATT ATT CAC AGG GAT TTA	637
Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu	
175 180 185 190	
AAA CCA AGT AAC ATT GTA GTC AAG TCT GAT TGC ACA TTG AAA ATC CTG	685
Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu	
195 200 205	
GAC TTT GGA CTG GCC AGG ACA GCA GGC ACA AGC TTC ATG ATG ACT CCA	733
Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro	
210 215 220	
TAT GTG GTG ACA CGT TAT TAC AGA GCC CCT GAG GTC ATC CTG GGG ATG	781
Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met	
225 230 235	

GGC TAC AAG GAG AAC GTG GAT ATA TGG TCT GTG GGA TGC ATT ATG GGA Gly Tyr Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly 240 245 250	829
GAA ATG GTT CGC CAC AAA ATC CTC TTT CCA GGA AGG GAC TAT ATT GAC Glu Met Val Arg His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile Asp 255 260 265 270	877
CAG TGG AAT AAG GTA ATT GAA CAA CTA GGA ACA CCA TGT CCA GAA TTC Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe 275 280 285	925
ATG AAG AAA TTG CAA CCC ACA GTA AGA AAC TAT GTG GAG AAT CGG CCC Met Lys Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro 290 295 300	973
AAG TAT GCG GGA CTC ACC TTC CCC AAA CTC TTC CCA GAT TCC CTC TTC Lys Tyr Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe 305 310 315	1021
CCA GCG GAC TCC GAG CAC AAT AAA CTC AAA GCC AGC CAA GCC AGG GAC Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp 320 325 330	1069
TTG TTG TCA AAG ATG CTA GTG ATT GAC CCA GCA AAA AGA ATA TCA GTG Leu Leu Ser Lys Met Leu Val Ile Asp Pro Ala Lys Arg Ile Ser Val 335 340 345 350	1117
GAC GAC GCC TTA CAG CAT CCC TAC ATC AAC GTC TGG TAT GAC CCA GCC Asp Asp Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala 355 360 365	1165
GAA GTG GAG GCG CCT CCA CCT CAG ATA TAT GAC AAG CAG TTG GAT GAA Glu Val Glu Ala Pro Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu 370 375 380	1213
AGA GAA CAC ACA ATT GAA GAA TGG AAA GAA CTT ATC TAC AAG GAA GTA Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val 385 390 395	1261
ATG AAT TCA GAA GAA AAG ACT AAA AAT GGT GTA GTA AAA GGA CAG CCT Met Asn Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro 400 405 410	1309
TCT CCT TCA GGT GCA GCA GTG AAC AGC AGT GAG AGT CTC CCT CCA TCC Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser 415 420 425 430	1357
TCG TCT GTC AAT GAC ATC TCC TCC ATG TCC ACC GAC CAG ACC CTG GCA Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala 435 440 445	1405
TCT GAC ACT GAC AGC AGC CTG GAA GCC TCG GCA GGA CCC CTG GGT TGT Ser Asp Thr Asp Ser Ser Leu Glu Ala Ser Ala Gly Pro Leu Gly Cys 450 455 460	1453
TGC AGG TGACTAGCCG CCTGCCTGCG AAACCCAGCG TTCTTCAGGA GATGAT Cys Arg	1505

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Leu	His	Phe	Leu	Tyr	Tyr	Cys	Ser	Glu	Pro	Thr	Leu	Asp	Val
1				5					10					15	
Lys	Ile	Ala	Phe	Cys	Gln	Gly	Phe	Asp	Lys	Gln	Val	Asp	Val	Ser	Tyr
			20					25					30		
Ile	Ala	Lys	His	Tyr	Asn	Met	Ser	Lys	Ser	Lys	Val	Asp	Asn	Gln	Phe
		35					40					45			
Tyr	Ser	Val	Glu	Val	Gly	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr
	50					55					60				
Gln	Asn	Leu	Lys	Pro	Ile	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala
65					70					75				80	
Ala	Tyr	Asp	Ala	Val	Leu	Asp	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser
			85					90						95	
Arg	Pro	Phe	Gln	Asn	Gln	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu
		100						105					110		
Val	Leu	Met	Lys	Cys	Val	Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn
	115					120						125			
Val	Phe	Thr	Pro	Gln	Lys	Thr	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Leu
	130					135					140				
Val	Met	Glu	Leu	Met	Asp	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu
145					150					155				160	
Leu	Asp	His	Glu	Arg	Met	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly
			165					170					175		
Ile	Lys	His	Leu	His	Ser	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro
		180					185						190		
Ser	Asn	Ile	Val	Val	Lys	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe
	195						200					205			
Gly	Leu	Ala	Arg	Thr	Ala	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val
	210					215					220				
Val	Thr	Arg	Tyr	Tyr	Arg	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr
225					230					235				240	
Lys	Glu	Asn	Val	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met
			245						250				255		
Val	Arg	His	Lys	Ile	Leu	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp
		260						265					270		
Asn	Lys	Val	Ile	Glu	Gln	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys
	275						280					285			
Lys	Leu	Gln	Pro	Thr	Val	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr
	290					295					300				
Ala	Gly	Leu	Thr	Phe	Pro	Lys	Leu	Phe	Pro	Asp	Ser	Leu	Phe	Pro	Ala
305					310					315				320	
Asp	Ser	Glu	His	Asn	Lys	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu
			325					330					335		
Ser	Lys	Met	Leu	Val	Ile	Asp	Pro	Ala	Lys	Arg	Ile	Ser	Val	Asp	Asp
		340						345					350		
Ala	Leu	Gln	His	Pro	Tyr	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Val
	355						360					365			
Glu	Ala	Pro	Pro	Pro	Gln	Ile	Tyr	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu
	370					375					380				

His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn
 385 390 395 400
 Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro
 405 410 415
 Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser
 420 425 430
 Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp
 435 440 445
 Thr Asp Ser Ser Leu Glu Ala Ser Ala Gly Pro Leu Gly Cys Cys Arg
 450 455 460

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGAAATGGC	GTGGCAGGGG	ACCCAGCGAG	CCCAGAGGGA	TTTTGCCGCT	GCTTCCTCTA	60
CCCCTGTATT	TCACGCAGCT	CTCTAAATTG	ACTCAGCTCC	AGGCTAGTGT	GAGAAACACC	120
AACAGCAGGC	CCATCTCAGA	TCTTCACTAT	GGCAACTTAT	GCAAGAAACT	GTTGAATTAG	180
ACCCGTTTCC	TATAGATGAG	AAACCATACA	AGCTGTGGTA	TTTATGAGCC	TCCATTTCTT	240
ATACTACTGC	AGTGAACCAA	CATTGGATGT	GAAAATTGCC	TTTTGTCCAGG	GATTCGATAA	300
ACAAGTGGAT	GTGTCAATATA	TTGCCAAACA	TTACAACATG	AGCAAAAGCA	AAGTTGACAA	360
CCAGTTCTAC	AGTGTGGAAG	TGGGAGACTC	AACCTTCACA	GTTCTCAAGC	GCTACCAGAA	420
TCTAAAGCCT	ATTGGCTCTG	GGGCTCAGGG	CATAGTTTGT	GCCGCGTATG	ATGCTGTCCT	480
TGACAGAAAT	GTGGCCATTA	AGAAGCTCAG	CAGACCCTTT	CAGAACCAAA	CACATGCCAA	540
GAGAGCGTAC	CGGGAGCTGG	TCCTCATGAA	GTGTGTGAAC	CATAAAAACA	TTATTAGTTT	600
ATTAAATGTC	TTCACACCCC	AGAAAACGCT	GGAGGAGTTC	CAAGATGTTT	ACTTAGTAAT	660
GGAAGTATG	GATGCCAACT	TATGTCAAGT	GATTCAGATG	GAATTAGACC	ATGAGCGAAT	720
GTCTTACCTG	CTGTACCAAA	TGTTGTGTGG	CATTAAGCAC	CTCCATTCTG	CTGGAATTAT	780
TCACAGGGAT	TTAAAACCAA	GTAACATTGT	AGTCAAGTCT	GATTGCACAT	TGAAAATCCT	840
GGACTTTTGA	CTGGCCAGGA	CAGCAGGCAC	AAGCTTCATG	ATGACTCCAT	ATGTGGTGAC	900
ACGTTATTAC	AGAGCCCCTG	AGGTCATCCT	GGGATGGGGC	TACAAGGAGA	ACGTGGATAT	960
ATGGTCTGTG	GGATGCATTA	TGGGAGAAAT	GGTTCGCCAC	AAAATCCTCT	TTCCAGGAAG	1020
GGACTATATT	GACCAAGTGA	ATAAGGTAAT	TGAACAACTA	GGAACACCAT	GTCCAGAATT	1080
CATGAAGAAA	TTGCAACCCA	CAGTAAGAAA	CTATGTGGAG	AATCGGCCCA	AGTATGCGGG	1140
ACTCACCTTC	CCCAAACCTC	TCCCAGATTG	CCTCTTCCCA	GCGGACTCCG	AGCACAATAA	1200
ACTCAAAGCC	AGCCAAGCCA	GGGACTTGTT	GTCAAAGATG	CTAGTGATTG	ACCCAGCAAA	1260
AAGAATATCA	GTGGACGACG	CCTTACAGCA	TCCCTACATC	AACGTCTGGT	ATGACCCAGC	1320
CGAAGTGGAG	GCGCCTCCAC	CTCAGATATA	TGACAAGCAG	TTGGATGAAA	GAGAACACAC	1380
AATTGAAGAA	TGGAAGAAGC	TTATCTACAA	GGAAGTAATG	AATTCAGAAG	AAAAGACTAA	1440
AAATGGTGTA	GTAAAAGGAC	AGCCTTCTCC	TTCAGGTGCA	GCAGTGAACA	GCAGTGAGAG	1500
TCTCCCTCCA	TCCTCGTCTG	TCAATGACAT	CTCCTCCATG	TCCACCGACC	AGACCTGGC	1560
ATCTGACACT	GACAGCAGCC	TGGAAGCCTC	GGCAGGACCC	CTGGGTGTGT	GCAGGTGACT	1620
AGCCGCCTGC	CTGCGAAACC	CAGCGTTCTT	CAGGAGATGA	TGTGATGGAA	CACACACACA	1680
CGCAGACACA	CACACACACA	CAAATGCAGA	CACACAACAT	CAAGAAAACA	GCAAGGGAGA	1740
GAATCCAAGC	CTAAAATTAA	ATAAATCTTT	CAGCCTGCTT	CTTCCCAGG	GTTCTGTATT	1800
GCAGCTAAGC	TCAAATGTAT	ATTTAACTTC	TAGTTGCTCT	TGCTTTGGTC	TTCTTCCAAT	1860
GATGCTTACT	ACAGAAAGCA	AATCAGACAC	AATTAGAGAA	GCCTTTTCCA	TAAAGTGATA	1920
TTTAAATGGC	TGCAAAACCG	GCAACCTGTA	ACTGCCCTTT	TAAATGGCAT	GACAAGGTGT	1980
GCAAGTGGCC	CATCCAGCAT	GTGTGTGTCT	CTATCTTGCA	TCTACCTGCT	CCTTGGCCTA	2040
GTCAGATGGA	TGTAGATACA	GATCCGCATG	TGTCTGTATT	CATACAGCAC	TACTTACTTA	2100
GAGATGCTAC	TCTCAGTGTC	CTCAGGGCTC	TACCAAGACA	TAATGCACTG	GGGTACCACA	2160
TGGTCCATTT	CATGTGATCT	ATTACTCTGA	CATAAACCCA	TCTGTAATAT	ATTGCCAGTA	2220
TATAAGCTGT	TTAGTTTGTG	AATTGATTAA	ACTGTATGTC	TTATAAGAAA	ACATGTAAAG	2280

GGGGAATATA TTGGGGGAGT GAGCTCTCTC AGACCCTTGA AGATGTAGCT TCCAAATTG
AATGGATTAA ATGGCACCTG TATACCA

2340
2367

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 92...1357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCTCAGATC TTCACTATGG CAACTTATGC AAGAACTGT TGAATTAGAC CCGTTTCCTA	60
TAGATGAGAA ACCATACAAG CTGTGGTATT T ATG AGC CTC CAT TTC TTA TAC	112
Met Ser Leu His Phe Leu Tyr	
1 5	
TAC TGC AGT GAA CCA ACA TTG GAT GTG AAA ATT GCC TTT TGT CAG GGA	160
Tyr Cys Ser Glu Pro Thr Leu Asp Val Lys Ile Ala Phe Cys Gln Gly	
10 15 20	
TTC GAT AAA CAA GTG GAT GTG TCA TAT ATT GCC AAA CAT TAC AAC ATG	208
Phe Asp Lys Gln Val Asp Val Ser Tyr Ile Ala Lys His Tyr Asn Met	
25 30 35	
AGC AAA AGC AAA GTT GAC AAC CAG TTC TAC AGT GTG GAA GTG GGA GAC	256
Ser Lys Ser Lys Val Asp Asn Gln Phe Tyr Ser Val Glu Val Gly Asp	
40 45 50 55	
TCA ACC TTC ACA GTT CTC AAG CGC TAC CAG AAT CTA AAG CCT ATT GGC	304
Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile Gly	
60 65 70	
TCT GGG GCT CAG GGC ATA GTT TGT GCC GCG TAT GAT GCT GTC CTT GAC	352
Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Val Leu Asp	
75 80 85	
AGA AAT GTG GCC ATT AAG AAG CTC AGC AGA CCC TTT CAG AAC CAA ACA	400
Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln Thr	
90 95 100	
CAT GCC AAG AGA GCG TAC CGG GAG CTG GTC CTC ATG AAG TGT GTG AAC	448
His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val Asn	
105 110 115	
CAT AAA AAC ATT ATT AGT TTA TTA AAT GTC TTC ACA CCC CAG AAA ACG	496
His Lys Asn Ile Ile Ser Leu Leu Asn Val Phe Thr Pro Gln Lys Thr	
120 125 130 135	
CTG GAG GAG TTC CAA GAT GTT TAC TTA GTA ATG GAA CTG ATG GAT GCC	544
Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met Glu Leu Met Asp Ala	
140 145 150	

AAC TTA TGT CAA GTG ATT CAG ATG GAA TTA GAC CAT GAG CGA ATG TCT	592
Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met Ser	
155 160 165	
TAC CTG CTG TAC CAA ATG TTG TGT GGC ATT AAG CAC CTC CAT TCT GCT	640
Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser Ala	
170 175 180	
GGA ATT ATT CAC AGG GAT TTA AAA CCA AGT AAC ATT GTA GTC AAG TCT	688
Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys Ser	
185 190 195	
GAT TGC ACA TTG AAA ATC CTG GAC TTT GGA CTG GCC AGG ACA GCA GGC	736
Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala Gly	
200 205 210 215	
ACA AGC TTC ATG ATG ACT CCA TAT GTG GTG ACA CGT TAT TAC AGA GCC	784
Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr Arg Ala	
220 225 230	
CCT GAG GTC ATC CTG GGG ATG GGC TAC AAG GAG AAC GTG GAT ATA TGG	832
Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp Ile Trp	
235 240 245	
TCT GTG GGA TGC ATT ATG GGA GAA ATG GTT CGC CAC AAA ATC CTC TTT	880
Ser Val Gly Cys Ile Met Gly Glu Met Val Arg His Lys Ile Leu Phe	
250 255 260	
CCA GGA AGG GAC TAT ATT GAC CAG TGG AAT AAG GTA ATT GAA CAA CTA	928
Pro Gly Arg Asp Tyr Ile Asp Gln Trp Asn Lys Val Ile Glu Gln Leu	
265 270 275	
GGA ACA CCA TGT CCA GAA TTC ATG AAG AAA TTG CAA CCC ACA GTA AGA	976
Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr Val Arg	
280 285 290 295	
AAC TAT GTG GAG AAT CGG CCC AAG TAT GCG GGA CTC ACC TTC CCC AAA	1024
Asn Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Leu Thr Phe Pro Lys	
300 305 310	
CTC TTC CCA GAT TCC CTC TTC CCA GCG GAC TCC GAG CAC AAT AAA CTC	1072
Leu Phe Pro Asp Ser Leu Phe Pro Ala Asp Ser Glu His Asn Lys Leu	
315 320 325	
AAA GCC AGC CAA GCC AGG GAC TTG TTG TCA AAG ATG CTA GTG ATT GAC	1120
Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val Ile Asp	
330 335 340	
CCA GCA AAA AGA ATA TCA GTG GAC GAC GCC TTA CAG CAT CCC TAC ATC	1168
Pro Ala Lys Arg Ile Ser Val Asp Asp Ala Leu Gln His Pro Tyr Ile	
345 350 355	
AAC GTC TGG TAT GAC CCA GCC GAA GTG GAG GCG CCT CCA CCT CAG ATA	1216
Asn Val Trp Tyr Asp Pro Ala Glu Val Glu Ala Pro Pro Pro Gln Ile	
360 365 370 375	
TAT GAC AAG CAG TTG GAT GAA AGA GAA CAC ACA ATT GAA GAA TGG AAA	1264
Tyr Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp Lys	
380 385 390	

GAA CTT ATC TAC AAG GAA GTA ATG AAT TCA GAA GAA AAG ACT AAA AAT	1312
Glu Leu Ile Tyr Lys Glu Val Met Asn Ser Glu Glu Lys Thr Lys Asn	
395 400 405	
GGT GTA GTA AAA GGA CAG CCT TCT CCT TCA GCA CAG GTG CAG CAG	1357
Gly Val Val Lys Gly Gln Pro Ser Pro Ser Ala Gln Val Gln Gln	
410 415 420	
TGAACAGCAG TGAGAGTCTC CCTCCATCCT CGTCTGTCAA TGACATCTCC TCCATGTCCA	1417
CCGACCAGAC CCTGGCATCT GACACTGACA GCAGCCTGGA AGCCTCGGCA GGACCCCTGG	1477
GTTGTTGCAG GTGACTAGCC GCCTGCCTGC GAAACCCAGC GTTCTTCAGG AGATGATGTG	1537
ATGGAACACA CACACACGCA GACACACACA CACACACAAA TGCAGACACA CAACATCAAG	1597
AAAACAGCAA GGGAGAGAAT CCAAGCCTAA AATTAAATAA ATCTTTCAGC CTGCTTCTTC	1657
CCCAGGGTTC TGTATTGCAG CTAAGCTCAA ATGTATATTT AACTTCTAGT TGCTCTTGCT	1717
TTGGTCTTCT TCCAATGATG CTTACTACAG AAAGCAAATC AGACACAATT AGAGAA	1773

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 422 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ser	Leu	His	Phe	Leu	Tyr	Tyr	Cys	Ser	Glu	Pro	Thr	Leu	Asp	Val
1				5				10						15	
Lys	Ile	Ala	Phe	Cys	Gln	Gly	Phe	Asp	Lys	Gln	Val	Asp	Val	Ser	Tyr
		20						25					30		
Ile	Ala	Lys	His	Tyr	Asn	Met	Ser	Lys	Ser	Lys	Val	Asp	Asn	Gln	Phe
		35					40					45			
Tyr	Ser	Val	Glu	Val	Gly	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr
	50				55					60					
Gln	Asn	Leu	Lys	Pro	Ile	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala
65				70				75						80	
Ala	Tyr	Asp	Ala	Val	Leu	Asp	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser
			85					90						95	
Arg	Pro	Phe	Gln	Asn	Gln	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu
		100					105						110		
Val	Leu	Met	Lys	Cys	Val	Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn
	115					120					125				
Val	Phe	Thr	Pro	Gln	Lys	Thr	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Leu
	130					135					140				
Val	Met	Glu	Leu	Met	Asp	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu
145				150				155						160	
Leu	Asp	His	Glu	Arg	Met	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly
			165					170						175	
Ile	Lys	His	Leu	His	Ser	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro
		180					185						190		
Ser	Asn	Ile	Val	Val	Lys	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe
	195					200						205			
Gly	Leu	Ala	Arg	Thr	Ala	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val
	210				215					220					
Val	Thr	Arg	Tyr	Tyr	Arg	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr
225				230				235						240	
Lys	Glu	Asn	Val	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met
			245					250						255	

Val	Arg	His	Lys	Ile	Leu	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp
			260					265					270		
Asn	Lys	Val	Ile	Glu	Gln	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys
		275					280					285			
Lys	Leu	Gln	Pro	Thr	Val	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr
	290					295					300				
Ala	Gly	Leu	Thr	Phe	Pro	Lys	Leu	Phe	Pro	Asp	Ser	Leu	Phe	Pro	Ala
305					310					315				320	
Asp	Ser	Glu	His	Asn	Lys	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu
			325						330					335	
Ser	Lys	Met	Leu	Val	Ile	Asp	Pro	Ala	Lys	Arg	Ile	Ser	Val	Asp	Asp
		340						345					350		
Ala	Leu	Gln	His	Pro	Tyr	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Val
	355						360					365			
Glu	Ala	Pro	Pro	Pro	Gln	Ile	Tyr	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu
370						375					380				
His	Thr	Ile	Glu	Glu	Trp	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asn
385					390					395				400	
Ser	Glu	Glu	Lys	Thr	Lys	Asn	Gly	Val	Val	Lys	Gly	Gln	Pro	Ser	Pro
				405				410						415	
Ser	Ala	Gln	Val	Gln	Gln										
			420												

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGAAATGGC	GTGGCAGGGG	ACCCAGCGAG	CCCAGAGGGA	TTTTGCCGCT	GCTTCCTCTA	60
CCCCTGTATT	TCACGCAGCT	CTCTAAATTG	ACTCAGCTCC	AGGCTAGTGT	GAGAAACACC	120
AACAGCAGGC	CCATCTCAGA	TCTTCACTAT	GGCAACTTAT	GCAAGAAACT	GTTGAATTAG	180
ACCCGTTTTCC	TATAGATGAG	AAACCATACA	AGCTGTGGTA	TTTATGAGCC	TCCATTTCTT	240
ATACTACTGC	AGTGAACCAA	CATTGGATGT	GAAAATTGCC	TTTTGTCAGG	GATTCGATAA	300
ACAAGTGGAT	GTGTCATATA	TTGCCAAACA	TTACAACATG	AGCAAAAGCA	AAGTTGACAA	360
CCAGTTCTAC	AGTGTGGAAG	TGGGAGACTC	AACCTTCACA	GTTCTCAAGC	GCTACCAGAA	420
TCTAAAGCCT	ATTGGCTCTG	GGGCTCAGGG	CATAGTTTGT	GCCGCGTATG	ATGCTGTCCT	480
TGACAGAAAT	GTGGCCATTA	AGAAGCTCAG	CAGACCCTTT	CAGAACCAAA	CACATGCCAA	540
GAGAGCGTAC	CGGGAGCTGG	TCCTCATGAA	GTGTGTGAAC	CATAAAAACA	TTATTAGTTT	600
ATTAAATGTC	TTCACACCCC	AGAAAACGCT	GGAGGAGTTC	CAAGATGTTT	ACTTAGTAAT	660
GGAAGTGATG	GATGCCAACT	TATGTCAAGT	GATTCAGATG	GAATTAGACC	ATGAGCGAAT	720
GTCTTACCTG	CTGTACCAAA	TGTTGTGTGG	CATTAAGCAC	CTCCATTCTG	CTGGAATTAT	780
TCACAGGGAT	TTAAAACCAA	GTAACATTGT	AGTCAAGTCT	GATTGCACAT	TGAAAATCCT	840
GGACTTTGGA	CTGGCCAGGA	CAGCAGGCAC	AAGCTTCATG	ATGACTCCAT	ATGTGGTGAC	900
ACGTTATTAC	AGAGCCCCTG	AGGTCATCCT	GGGGATGGGC	TACAAGGAGA	ACGTGGATAT	960
ATGGTCTGTG	GGATGCATTA	TGGGAGAAAT	GGTTCGCCAC	AAAATCCTCT	TTCCAGGAAG	1020
GGACTATATT	GACCAGTGGA	ATAAGGTAAT	TGAACAACTA	GGAACACCAT	GTCCAGAATT	1080
CATGAAGAAA	TTGCAACCCA	CAGTAAGAAA	CTATGTGGAG	AATCGGCCCA	AGTATGCGGG	1140
ACTCACCTTC	CCCAAACCTC	TCCCAGATTC	CCTCTTCCCA	GCGGACTCCG	AGCACAATAA	1200
ACTCAAAGCC	AGCCAAGCCA	GGGACTTGTT	GTCAAAGATG	CTAGTGATTG	ACCCAGCAAA	1260
AAGAATATCA	GTGGACGACG	CCTTACAGCA	TCCCTACATC	AACGTCTGGT	ATGACCCAGC	1320
CGAAGTGGAG	GCGCCTCCAC	CTCAGATATA	TGACAAGCAG	TTGGATGAAA	GAGAACACAC	1380
AATTGAAGAA	TGGAAGAAGC	TTATCTACAA	GGAAGTAATG	AATTCAGAAG	AAAAGACTAA	1440
AAATGGTGTA	GTAAAAGGAC	AGCCTTCTCC	TTCAGCACAG	GTGCAGCAGT	GAACAGCAGT	1500
GAGAGTCTCC	CTCCATCTCC	GTCTGTCAAT	GACATCTCCT	CCATGTCCAC	CGACCAGACC	1560
CTGGCATCTG	ACACTGACAG	CAGCCTGGAA	GCCTCGGCAG	GACCCCTGGG	TTGTTGCAGG	1620

TGACTAGCCG	CCTGCCTGCG	AAACCCAGCG	TTCTTCAGGA	GATGATGTGA	TGGAACACAC	1680
ACACACGCAG	ACACACACAC	ACACACAAAT	GCAGACACAC	AACATCAAGA	AAACAGCAAG	1740
GGAGAGAATC	CAAGCCTAAA	ATTAAATAAA	TCTTTCAGCC	TGCTTCTTCC	CCAGGGTTCT	1800
GTATTGCAGC	TAAGCTCAAA	TGTATATTTA	ACTTCTAGTT	GCTCTTGCTT	TGGTCTTCTT	1860
CCAATGATGC	TTACTACAGA	AAGCAAATCA	GACACAATTA	GAGAAGCCTT	TTCCATAAAG	1920
TGTAATTTTA	ATGGCTGCAA	AACCGGCAAC	CTGTAAGTGC	CCTTTTAAAT	GGCATGACAA	1980
GGTGTGCAGT	GGCCCCATCC	AGCATGTGTG	TGTCTCTATC	TTGCATCTAC	CTGCTCCTTG	2040
GCCTAGTCAG	ATGGATGTAG	ATACAGATCC	GCATGTGTCT	GTATTCATAC	AGCACTACTT	2100
ACTTAGAGAT	GCTACTCTCA	GTGTCCTCAG	GGCTCTACCA	AGACATAATG	CACTGGGGTA	2160
CCACATGGTC	CATTTTCATGT	GATCTATTAC	TCTGACATAA	ACCCATCTGT	AATATATTGC	2220
CAGTATATAA	GCTGTTTAGT	TTGTTAATTG	ATTAAACTGT	ATGTCTTATA	AGAAAACATG	2280
TAAAGGGGGA	ATATATTGGG	GGAGTGAGCT	CTCTCAGACC	CTTGAAGATG	TAGCTTCCAA	2340
ATTTGAATGG	ATTAAATGGC	ACCTGTATAC	CA			2372

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 224...1489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGAAATGGC	GTGGCAGGGG	ACCCAGCGAG	CCCAGAGGGA	TTTTGCCGCT	GCTTCCTCTA	60
CCCCTGTATT	TCACGCAGCT	CTCTAAATTG	ACTCAGCTCC	AGGCTAGTGT	GAGAAACACC	120
AACAGCAGGC	CCATCTCAGA	TCTTCACTAT	GGCAACTTAT	GCAAGAAACT	GTTGAATTAG	180
ACCCGTTTCC	TATAGATGAG	AAACCATACA	AGCTGTGGTA	TTT ATG AGC CTC CAT		235
				Met Ser Leu His		
				1		
TTC TTA TAC TAC TGC AGT GAA CCA ACA TTG GAT GTG AAA ATT GCC TTT						283
Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu Asp Val Lys Ile Ala Phe						
5 10 15 20						
TGT CAG GGA TTC GAT AAA CAA GTG GAT GTG TCA TAT ATT GCC AAA CAT						331
Cys Gln Gly Phe Asp Lys Gln Val Asp Val Ser Tyr Ile Ala Lys His						
25 30 35						
TAC AAC ATG AGC AAA AGC AAA GTT GAC AAC CAG TTC TAC AGT GTG GAA						379
Tyr Asn Met Ser Lys Ser Lys Val Asp Asn Gln Phe Tyr Ser Val Glu						
40 45 50						
GTG GGA GAC TCA ACC TTC ACA GTT CTC AAG CGC TAC CAG AAT CTA AAG						427
Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys						
55 60 65						
CCT ATT GGC TCT GGG GCT CAG GGC ATA GTT TGT GCC GCG TAT GAT GCT						475
Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala						
70 75 80						
GTC CTT GAC AGA AAT GTG GCC ATT AAG AAG CTC AGC AGA CCC TTT CAG						523
Val Leu Asp Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln						
85 90 95 100						

AAC CAA ACA CAT GCC AAG AGA GCG TAC CGG GAG CTG GTC CTC ATG AAG	571
Asn Gln Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys	
105 110 115	
TGT GTG AAC CAT AAA AAC ATT ATT AGT TTA TTA AAT GTC TTC ACA CCC	619
Cys Val Asn His Lys Asn Ile Ile Ser Leu Leu Asn Val Phe Thr Pro	
120 125 130	
CAG AAA ACG CTG GAG GAG TTC CAA GAT GTT TAC TTA GTA ATG GAA CTG	667
Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met Glu Leu	
135 140 145	
ATG GAT GCC AAC TTA TGT CAA GTG ATT CAG ATG GAA TTA GAC CAT GAG	715
Met Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu	
150 155 160	
CGA ATG TCT TAC CTG CTG TAC CAA ATG TTG TGT GGC ATT AAG CAC CTC	763
Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu	
165 170 175 180	
CAT TCT GCT GGA ATT ATT CAC AGG GAT TTA AAA CCA AGT AAC ATT GTA	811
His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val	
185 190 195	
GTC AAG TCT GAT TGC ACA TTG AAA ATC CTG GAC TTT GGA CTG GCC AGG	859
Val Lys Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg	
200 205 210	
ACA GCA GGC ACA AGC TTC ATG ATG ACT CCA TAT GTG GTG ACA CGT TAT	907
Thr Ala Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr	
215 220 225	
TAC AGA GCC CCT GAG GTC ATC CTG GGG ATG GGC TAC AAG GAG AAC GTG	955
Tyr Arg Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val	
230 235 240	
GAT ATA TGG TCT GTG GGA TGC ATT ATG GGA GAA ATG GTT CGC CAC AAA	1003
Asp Ile Trp Ser Val Gly Cys Ile Met Gly Glu Met Val Arg His Lys	
245 250 255 260	
ATC CTC TTT CCA GGA AGG GAC TAT ATT GAC CAG TGG AAT AAG GTA ATT	1051
Ile Leu Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp Asn Lys Val Ile	
265 270 275	
GAA CAA CTA GGA ACA CCA TGT CCA GAA TTC ATG AAG AAA TTG CAA CCC	1099
Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro	
280 285 290	
ACA GTA AGA AAC TAT GTG GAG AAT CGG CCC AAG TAT GCG GGA CTC ACC	1147
Thr Val Arg Asn Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Leu Thr	
295 300 305	
TTC CCC AAA CTC TTC CCA GAT TCC CTC TTC CCA GCG GAC TCC GAG CAC	1195
Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe Pro Ala Asp Ser Glu His	
310 315 320	
AAT AAA CTC AAA GCC AGC CAA GCC AGG GAC TTG TTG TCA AAG ATG CTA	1243
Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu	
325 330 335 340	

GTG ATT GAC CCA GCA AAA AGA ATA TCA GTG GAC GAC GCC TTA CAG CAT	1291
Val Ile Asp Pro Ala Lys Arg Ile Ser Val Asp Asp Ala Leu Gln His	
345 350 355	
CCC TAC ATC AAC GTC TGG TAT GAC CCA GCC GAA GTG GAG GCG CCT CCA	1339
Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala Glu Val Glu Ala Pro Pro	
360 365 370	
CCT CAG ATA TAT GAC AAG CAG TTG GAT GAA AGA GAA CAC ACA ATT GAA	1387
Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu	
375 380 385	
GAA TGG AAA GAA CTT ATC TAC AAG GAA GTA ATG AAT TCA GAA GAA AAG	1435
Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn Ser Glu Glu Lys	
390 395 400	
ACT AAA AAT GGT GTA GTA AAA GGA CAG CCT TCT CCT TCA GCA CAG GTG	1483
Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro Ser Ala Gln Val	
405 410 415 420	
CAG CAG TGAACAGCAG TGAGAGTCTC CCTCCATCCT CGTCTGTCAA TGACATCTCC	1539
Gln Gln	

TCCATGTCCA CCGACCAGAC CCTGGCATCT GACACTGACA GCAGCCTGGA AGCCTCGGCA	1599
GGACCCCTGG GTTGTTCAGG GTGACTAGCC GCCTGCCTGC GAAACCCAGC GTTCTTCAGG	1659
AGATGATGTG ATGGAACACA CACACACGCA GACACACACA CACACACAAA TGCAGACACA	1719
CAACATCAAG AAAACAGCAA GGGAGAGAAT CCAAGCCTAA AATTAAATAA ATCTTTCAGC	1779
CTGCTTCTTC CCCAGGGTTC TGTATTGCAG CTAAGCTCAA ATGTATATTT AACTTCTAGT	1839
TGCTCTTGCT TTGGTCTTCT TCCAATGATG CTTACTACAG AAAGCAAATC AGACACAATT	1899
AGAGAAGCCT TTTCCATAAA GTGTAATTTT AATGGCTGCA AAACCGGCAA CCTGTAAC TG	1959
CCCTTTTAAA TGGCATGACA AGGTGTGCAG TGGCCCCATC CAGCATGTGT GTGTCTCTAT	2019
CTTGTCATCTA CCTGCTCCTT GGCCTAGTCA GATGGATGTA GATACAGATC CGCATGTGTC	2079
TGTATTCTATA CAGCACTACT TACTTAGAGA TGCTACTCTC AGTGTCTCTCA GGGCTCTACC	2139
AAGACATAAT GCACTGGGGT ACCACATGGT CCATTTTCATG TGATCTATTA CTCTGACATA	2199
AACCCATCTG TAATATATTG CCAGTATATA AGCTGTTTAG TTTGTTAATT GATTAAACTG	2259
TATGTCTTAT AAGAAAACAT GTAAAGGGGG AATATATTGG GGGAGTGAGC TCTCTCAGAC	2319
CCTTGAAGAT GTAGCTTCCA AATTTGAATG GATTAAATGG CACCTGTATA CCA	2372

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu Asp Val	
1 5 10 15	
Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val Ser Tyr	
20 25 30	
Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn Gln Phe	
35 40 45	
Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr	
50 55 60	
Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala	
65 70 75 80	

Ala	Tyr	Asp	Ala	Val	Leu	Asp	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser
				85					90					95	
Arg	Pro	Phe	Gln	Asn	Gln	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu
			100					105					110		
Val	Leu	Met	Lys	Cys	Val	Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn
		115				120						125			
Val	Phe	Thr	Pro	Gln	Lys	Thr	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Leu
	130				135						140				
Val	Met	Glu	Leu	Met	Asp	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu
145					150				155						160
Leu	Asp	His	Glu	Arg	Met	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly
			165					170						175	
Ile	Lys	His	Leu	His	Ser	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro
			180				185						190		
Ser	Asn	Ile	Val	Val	Lys	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe
	195					200						205			
Gly	Leu	Ala	Arg	Thr	Ala	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val
	210					215					220				
Val	Thr	Arg	Tyr	Tyr	Arg	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr
225					230					235					240
Lys	Glu	Asn	Val	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met
			245					250						255	
Val	Arg	His	Lys	Ile	Leu	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp
			260					265					270		
Asn	Lys	Val	Ile	Glu	Gln	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys
		275					280					285			
Lys	Leu	Gln	Pro	Thr	Val	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr
	290				295					300					
Ala	Gly	Leu	Thr	Phe	Pro	Lys	Leu	Phe	Pro	Asp	Ser	Leu	Phe	Pro	Ala
305					310					315					320
Asp	Ser	Glu	His	Asn	Lys	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu
			325					330					335		
Ser	Lys	Met	Leu	Val	Ile	Asp	Pro	Ala	Lys	Arg	Ile	Ser	Val	Asp	Asp
			340					345					350		
Ala	Leu	Gln	His	Pro	Tyr	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Val
		355					360					365			
Glu	Ala	Pro	Pro	Pro	Gln	Ile	Tyr	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu
	370					375					380				
His	Thr	Ile	Glu	Glu	Trp	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asn
385					390					395					400
Ser	Glu	Glu	Lys	Thr	Lys	Asn	Gly	Val	Val	Lys	Gly	Gln	Pro	Ser	Pro
			405					410					415		
Ser	Ala	Gln	Val	Gln	Gln										
					420										

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 364...1641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCTCCTTAT TCCGGTTTGG AATGTGGCTA ATGAAAGCCC AGTAGGAGGA TTTCTGGGGC

60

AAACAGGTGG	ACCAGGATCC	TGGTTCTCAG	GCACGGAATG	GCTATTGTGA	GAGCGCCACC	120
AGCAGGACCA	TCGCAGATCT	TGGTTATGGC	TGCTCACGCA	AGAGGCTGTT	GATGTAGACC	180
CCCTTTCCCG	TAGATGAGAA	ATCACACGAG	CAGTGGTATT	TATGAGCCTC	CATTTCTTAT	240
ACTACTGCAG	TGAACCAACC	TTGGATGTGA	AAATTGCCTT	TTGTCAGGTG	TGTGTTCCCTT	300
ACAGGTAAAA	CAAAGGGATT	CGACAAACAC	GTGGATGTGT	CTTCTGTTGT	CAAACATTAC	360
AAC ATG AGC AAA AGC AAG GTA GAT AAC CAG TTC	TAC AGT GTG GAA GTG	408				
Met Ser Lys Ser Lys Val Asp Asn Gln Phe	Tyr Ser Val Glu Val					
1	5	10	15			
GGA GAC TCA ACC TTC ACA GTT CTA AAG CGC TAC CAG AAC CTG AAG CCG	456					
Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro						
20	25	30				
ATC GGC TCT GGG GCT CAG GGA ATA GTT TGT GCT GCG TAT GAC GCT GTC	504					
Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Val						
35	40	45				
CTC GAC AGA AAT GTG GCC ATT AAG AAG CTC AGC AGA CCC TTC CAG AAC	552					
Leu Asp Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn						
50	55	60				
CAA ACT CAT GCC AAG AGG GCT TAC CGG GAG CTG GTC CTC ATG AAG TGT	600					
Gln Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys						
65	70	75				
GTG AAC CAT AAA AAC ATT ATT AGC TTA TTA AAT GTC TTT ACA CCC CAG	648					
Val Asn His Lys Asn Ile Ile Ser Leu Leu Asn Val Phe Thr Pro Gln						
80	85	90				
AAA ACA CTG GAG GAG TTC CAA GAT GTT TAC TTA GTG ATG GAA CTG ATG	696					
Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met Glu Leu Met						
100	105	110				
GAC GCC AAC TTG TGT CAG GTG ATT CAG ATG GAG CTG GAC CAC GAG CGG	744					
Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg						
115	120	125				
ATG TCG TAC TTG CTG TAC CAG ATG CTG TCG GCG ATC AAA CAC CTC CAC	792					
Met Ser Tyr Leu Leu Tyr Gln Met Leu Ser Ala Ile Lys His Leu His						
130	135	140				
TCC GCT GGG ATC ATC CAC AGG GAC TTA AAA CCC AGT AAC ATC GTA GTC	840					
Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val						
145	150	155				
AAG TCT GAT TGC ACA CTG AAA ATC CTG GAC TTT GGA CTG GCC AGG ACA	888					
Lys Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr						
160	165	170				
GCG GGC ACA AGC TTC ATG ATG ACT CCG TAT GTG GTG ACG AGA TAT TAC	936					
Ala Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr						
180	185	190				
AGA GCC CCC GAG GTC ATC CTG GGC ATG GGC TAC AAG GAG AAC GTG GAC	984					
Arg Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp						
195	200	205				
ATA TGG TCT GTG GGC TGC ATC ATG GGA GAA ATG GTT CGT CAC AAA ATC	1032					
Ile Trp Ser Val Gly Cys Ile Met Gly Glu Met Val Arg His Lys Ile						
210	215	220				

CTC TTT CCC GGA AGG GAC TAT ATT GAC CAG TGG AAC AAA GTC ATA GAG Leu Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp Asn Lys Val Ile Glu 225 230 235	1080
CAG CTA GGA ACT CCG TGT CCA GAA TTC ATG AAG AAA TTG CAG CCC ACC Gln Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr 240 245 250 255	1128
GTC AGA AAC TAC GTG GAG AAC CGG CCC AAG TAT GCA GGC CTC ACC TTC Val Arg Asn Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Leu Thr Phe 260 265 270	1176
CCC AAG CTC TTT CCA GAT TCC CTC TTC CCA GCG GAT TCC GAG CAC AAT Pro Lys Leu Phe Pro Asp Ser Leu Phe Pro Ala Asp Ser Glu His Asn 275 280 285	1224
AAA CTT AAA GCC AGC CAA GCC AGG GAC TTG TTG TCA AAG ATG TTA GTG Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val 290 295 300	1272
ATT GAC CCA GCG AAG AGG ATA TCG GTG GAT GAC GCA TTG CAG CAT CCG Ile Asp Pro Ala Lys Arg Ile Ser Val Asp Asp Ala Leu Gln His Pro 305 310 315	1320
TAC ATC AAC GTT TGG TAC GAC CCT GCT GAA GTG GAG GCG CCT CCG CCT Tyr Ile Asn Val Trp Tyr Asp Pro Ala Glu Val Glu Ala Pro Pro Pro 320 325 330 335	1368
CAG ATA TAT GAC AAG CAA TTG GAT GAA AGG GAG CAC ACC ATC GAA GAA Gln Ile Tyr Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu 340 345 350	1416
TGG AAA GAA CTC ATC TAC AAG GAA GTA ATG AAC TCA GAA GAG AAG ACT Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn Ser Glu Glu Lys Thr 355 360 365	1464
AAG AAC GGC GTA GTC AAA GGC CAG CCC TCA CCT TCA GGT GCA GCA GTG Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro Ser Gly Ala Ala Val 370 375 380	1512
AAC AGC AGT GAG AGT CTC CCT CCA TCC TCA TCT GTC AAC GAC ATC TCC Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser Val Asn Asp Ile Ser 385 390 395	1560
TCC ATG TCC ACC GAC CAG ACC CTC GCA TCC GAC ACT GAC AGC AGC CTG Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp Thr Asp Ser Ser Leu 400 405 410 415	1608
GAA GCC TCG GCG GGA CCG CTG GGT TGT TGC AGG TGACTAGCCG CCTGCCTGCG Glu Ala Ser Ala Gly Pro Leu Gly Cys Cys Arg 420 425	1661
AAACCCAGCG TTCTTCAGGA GATGACGCCA TGATAGAACA CAGCGCACAT GCACACACAC	1721
AGAGCTTGTA CACACACACA CACACACACA CACACGCACG CACGCACGCA CGCAAGCACG	1781
CACGCACGCA CAAATGCACT CACGCAATGT CAAGAAAAAA AAAAGTAGCG AGAGAGAGCG	1841
AGAGAGCCAA CGTAAACTA AGTTAAATCT TTCTGCGTGC TTCTCCAGAG TTCTGTATCG	1901
CAGCTGAGCT GAAATGTATA CTTAACTTCT AGTCGCGCTC GCTCGACTTT GGTCTCCCTC	1961
CGGCAGTGCT TACT	1975

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ser	Lys	Ser	Lys	Val	Asp	Asn	Gln	Phe	Tyr	Ser	Val	Glu	Val	Gly
1				5					10					15	
Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Asn	Leu	Lys	Pro	Ile
			20					25					30		
Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Tyr	Asp	Ala	Val	Leu
		35					40					45			
Asp	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln
	50					55					60				
Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Met	Lys	Cys	Val
	65				70					75					80
Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys
				85					90					95	
Thr	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Leu	Val	Met	Glu	Leu	Met	Asp
			100					105					110		
Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu	Leu	Asp	His	Glu	Arg	Met
		115					120					125			
Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Ser	Ala	Ile	Lys	His	Leu	His	Ser
	130					135					140				
Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys
	145				150					155					160
Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala
			165						170					175	
Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg
			180					185					190		
Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile
		195					200					205			
Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Val	Arg	His	Lys	Ile	Leu
	210					215					220				
Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln
	225				230					235					240
Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val
				245					250					255	
Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Leu	Thr	Phe	Pro
			260					265					270		
Lys	Leu	Phe	Pro	Asp	Ser	Leu	Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys
		275					280					285			
Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile
	290					295					300				
Asp	Pro	Ala	Lys	Arg	Ile	Ser	Val	Asp	Asp	Ala	Leu	Gln	His	Pro	Tyr
	305				310					315					320
Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Val	Glu	Ala	Pro	Pro	Pro	Gln
				325					330					335	
Ile	Tyr	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp
			340					345					350		
Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asn	Ser	Glu	Glu	Lys	Thr	Lys
		355					360					365			
Asn	Gly	Val	Val	Lys	Gly	Gln	Pro	Ser	Pro	Ser	Gly	Ala	Ala	Val	Asn
	370					375					380				

Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser Val Asn Asp Ile Ser Ser
 385 390 395 400
 Met Ser Thr Asp Gln Thr Leu Ala Ser Asp Thr Asp Ser Ser Leu Glu
 405 410 415
 Ala Ser Ala Gly Pro Leu Gly Cys Cys Arg
 420 425

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 310...1575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGCTTGAG TGAGCTAAAG ATTGGGTCTT CTTGGAAATC ACCTGTCTGT TATTATTTTT	60
AAACAATCGC TACACCTCCA AAGACTCTGC TCCTTACTCC GGTTTGGAAT GTGGCTAATG	120
ACTACCCAGT AGGGAGGATT TCTGGGGCAA ACAGCCGGAC CAGGATCCTA GTTCTCAGGC	180
ACGGAATGGC TATTGTGAGA ACAGCACCAG CAGGATCATC GCAGATCTTG GTTATGGCCA	240
CTCAGGCAAG ACGCTGTTGA GTTAAGACCC CTTTCCCATG GATGAGAAGC CACAGAAGCA	300
GTGGTATTT ATG AGC CTC CAT TTC TTA TAC TAC TGC AGT GAA CCA ACC TTG	351
Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu	
1 5 10	
GAT GTG AAA ATT GCC TTT TGT CAG GGA TTC GAT AAA CAC GTG GAT GTG	399
Asp Val Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys His Val Asp Val	
15 20 25 30	
TCA TCT ATT GCC AAA CAT TAC AAC ATG AGC AAA AGC AAG GTG GAC AAC	447
Ser Ser Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn	
35 40 45	
CAG TTC TAC AGT GTG GAA GTG GGG GAC TCA ACC TTC ACC GTT CTT AAG	495
Gln Phe Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys	
50 55 60	
CGC TAC CAG AAC CTG AAG CCA ATT GGC TCT GGG GCT CAG GGA ATA GTC	543
Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val	
65 70 75	
TGT GCT GCG TAC GAC GCT GTC CTT GAC AGA AAT GTG GCC ATT AAG AAG	591
Cys Ala Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys	
80 85 90	
CTC AGC AGA CCC TTC CAG AAC CAA ACT CAC GCC AAG AGG GCT TAC CGG	639
Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg	
95 100 105 110	
GAG CTG GTG CTC ATG AAG TGT GTG AAC CAT AAA AAC ATT ATT AGC TTA	687
Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu	
115 120 125	

TTA AAT GTT TTT ACA CCC CAG AAA ACG CTG GAG GAG TTC CAA GAT GTC Leu Asn Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val 130 135 140	735
TAC TTA GTG ATG GAA CTG ATG GAC GCC AAC CTG TGT CAG GTG ATT CAG Tyr Leu Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile Gln 145 150 155	783
ATG GAG CTG GAC CAC GAG CGG ATG TCT TAC TTG CTG TAC CAG ATG CTG Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Tyr Gln Met Leu 160 165 170	831
TGT GGC ATC AAG CAC CTC CAC TCC GCT GGG ATC ATC CAC AGG GAC TTA Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu 175 180 185 190	879
AAA CCC AGT AAC ATT GTA GTC AAG TCT GAT TGC ACA CTG AAA ATC CTC Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu 195 200 205	927
GAC TTC GGA CTG GCC AGG ACA GCG GGT ACA AGC TTC ATG ATG ACT CCG Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro 210 215 220	975
TAT GTG GTG ACG CGA TAT TAC AGA GCC CCT GAG GTC ATC CTG GGC ATG Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met 225 230 235	1023
GGC TAC AAG GAG AAC GTG GAC ATA TGG TCT GTG GGA TGC ATC ATG GGA Gly Tyr Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly 240 245 250	1071
GAA ATG GTT CGC CAC AAA ATC CTC TTT CCC GGA AGG AGC TAT ATT GAC Glu Met Val Arg His Lys Ile Leu Phe Pro Gly Arg Ser Tyr Ile Asp 255 260 265 270	1119
CAG TGG AAC AAA GTC ATC GAG CAG CTA GGA ACT CCG TGT CCA GAG TTC Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe 275 280 285	1167
ATG AAG AAA TTG CAG CCC ACA GTC AGA AAC TAC GTG GAG AAT CGG CCC Met Lys Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro 290 295 300	1215
AAG TAC GCA GGA CTC ACC TTC CCC AAG CTC TTT CCA GAT TCC CTC TTC Lys Tyr Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe 305 310 315	1263
CCA GCG GAT TCT GAG CAC AAT AAA CTT AAA GCC AGC CAA GCC AGG GAT Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp 320 325 330	1311
TTG TTG TCT AAG ATG TTA GTG ATT GAC CCA GTG AAG AGG ATA TCG GTG Leu Leu Ser Lys Met Leu Val Ile Asp Pro Val Lys Arg Ile Ser Val 335 340 345 350	1359
GAC GAC GCA CTG CAG CAT CCG TAC ATC AAC GTT TGG TAC GAC CCG GCT Asp Asp Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala 355 360 365	1407

GAA GTG GAG GCG CCT CCG CCT CAG ATA TAT GAT AAG CAG CTG GAT GAA	1455
Glu Val Glu Ala Pro Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu	
370 375 380	
AGG GAG CAC ACC ATC GAA GAA TGG AAA GAA CTT ATC TAC AAG GAG GTA	1503
Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val	
385 390 395	
ATG AAC TCA GAA GAG AAG ACT AAG AAT GGC GTA GTC AAA AGC CAG CCC	1551
Met Asn Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Ser Gln Pro	
400 405 410	
TCG CCT TCA GCA CAG GTG CAG CAG TGAACAGCAG TGAGAGTCTC CCTCCATCCT	1605
Ser Pro Ser Ala Gln Val Gln Gln	
415 420	
CGGCTGTCAA CGACATCTCC TCCATGTCCA CCGACCAGAC CCTCGCATCT GACACTGACA	1665
GCAGCCTGGA GGCCTCGGCG GGACCGTTGG GTTGTTGCAG GTGACTAGCC GCCTGCCTGC	1725
GAAACCCAGC GTTCTTCAGG AGATGACGCG ATAGAACACA GCACACATGC ACACACACAG	1785
CTTGCTCTCA CACACACTCA GCTTGCTCAC ACACACACAC ACACATACAC ACAAACACAC	1845
ACTGTCTCTC TCTCACACAC ACACACTGTC ACAACGCACT CACGAAAGGT CAAGAAAAAA	1905
ATAACAATAG AGAGATCCAA CATAAAATTA AGTTAAATTT TTCTGCGTGC TTCTCCAAAG	1965
TTCTGTATCA CAGCTGAGCT GAAATGTATA CTTAACTTCT AGTTGCGCTC GCTTTGGTTT	2025
CCCTCCAGCA GTGCTTACTA CACAAGACAA ATCAGACACA ATTAGAGAAA CCTTTCCTA	2085
AAGTGTAAC TAAGTGCTG CAGAACCAGC AACCTGTAAC TGCCCTTCAA ATGGCATGAG	2145
GAGGTGGGCA CGGGTCCGCG CCAGCATGTG TGTGTCTCTA TCTCGCGTCT ACCTGCTCTT	2205
CCGGCCTAGT CAGATGGATG TAGATACAGA TCCCGCATGT GTCTGTATT C AACAGCACT	2265
TAGAGATGCT CCTGTCA GTG TCCTCCAGGC TCCACCAAGA CACACACCGG GGTACCACAT	2325
GGTCCATTTT ATGTGATCTA TTA CTCTGAC ATAAATCCAT CTGTAATATA TTGCCAGTAT	2385
ATAAGCTGTT TAGTTTGTTA ATTGCTTAAG CTGTATGTCT TATAAGAGAC TATGTAAAGG	2445
GGGAAAATGG AGGCGTGAAC TCTCAGACCC TTGAAGATGT AGCTTCCGAA TTTGACCGTT	2505
AAATGGCACC GTATACC	2522

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ser	Leu	His	Phe	Leu	Tyr	Tyr	Cys	Ser	Glu	Pro	Thr	Leu	Asp	Val
1				5					10					15	
Lys	Ile	Ala	Phe	Cys	Gln	Gly	Phe	Asp	Lys	His	Val	Asp	Val	Ser	Ser
		20						25					30		
Ile	Ala	Lys	His	Tyr	Asn	Met	Ser	Lys	Ser	Lys	Val	Asp	Asn	Gln	Phe
		35					40					45			
Tyr	Ser	Val	Glu	Val	Gly	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr
	50				55						60				
Gln	Asn	Leu	Lys	Pro	Ile	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala
65					70					75				80	
Ala	Tyr	Asp	Ala	Val	Leu	Asp	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser
			85						90					95	
Arg	Pro	Phe	Gln	Asn	Gln	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu
		100						105					110		
Val	Leu	Met	Lys	Cys	Val	Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn
	115					120						125			

Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu
 130 135 140
 Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu
 145 150 155 160
 Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly
 165 170 175
 Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro
 180 185 190
 Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe
 195 200 205
 Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro Tyr Val
 210 215 220
 Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met Gly Tyr
 225 230 235 240
 Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly Glu Met
 245 250 255
 Val Arg His Lys Ile Leu Phe Pro Gly Arg Ser Tyr Ile Asp Gln Trp
 260 265 270
 Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe Met Lys
 275 280 285
 Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro Lys Tyr
 290 295 300
 Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe Pro Ala
 305 310 315 320
 Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu
 325 330 335
 Ser Lys Met Leu Val Ile Asp Pro Val Lys Arg Ile Ser Val Asp Asp
 340 345 350
 Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala Glu Val
 355 360 365
 Glu Ala Pro Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu Arg Glu
 370 375 380
 His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn
 385 390 395 400
 Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Ser Gln Pro Ser Pro
 405 410 415
 Ser Ala Gln Val Gln Gln
 420

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 615...1616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCAACTTTC	CTGACCCAGA	GGACCGGTAA	CAAGTGGCCG	GGAGCAACTT	TTGCAAATCT	60
CTTCTGCGCC	TTAAGGCTGC	CACCGAGACT	GTAAAGAAAA	GGAGAAGAGG	AACCTATACT	120
CATACCAGTT	CGCACAGGCC	TAAGTTGGGC	GAGGCCTAGC	CGCGGCTGCC	TAGCGTCCCC	180
CCCCCCTCA	CAGCGGAGGA	GGGGACAGTT	GTTGGAGGCC	GGGCGGCAGA	CCCGATCGCG	240
GGCCTCCACC	GAGAATTCCG	TGACGACTGG	TCAGCACCGC	CGGAGAGCCG	CTGTTGCTGG	300
GACTGGTCTG	CGGGCTCCAA	GGAACCGCTG	CTCCCCGAGA	GCGCTCCGTG	AGTGACCGCG	360

ACTTTTCAAA	GCTCGGCATC	GCGCGGAGTC	CTACCAACGT	GAGTGCTAGC	GGAGTCTTAA	420
CCCTGCGCTC	CCTGGAGCGA	ACTGGGGAGG	AGGGCTCAGG	GGGAAGCACT	GCCGTCTGGA	480
GCGCACGCTC	TAAACAAACT	TTGTTACAGA	AGCAGGGACG	CGCGGGTATC	CCCCCGCTTC	540
CCGGCGCGCT	GTTGCGGCCC	CGAAACTTCT	GCGCACAGCC	CAGGCTAACC	CCGCGTGAAG	600
TGACGGACCG	TTCT	ATG ACT GCA AAG	ATG GAA ACG	ACC TTC TAC GAC GAT		650
		Met Thr Ala Lys Met Glu Thr	Thr Phe Tyr Asp Asp			
	1		5	10		
GCC CTC AAC GCC TCG TTC CTC CAG TCC GAG AGC GGT GCC TAC GGC TAC						698
Ala Leu Asn Ala Ser Phe Leu Gln Ser Glu Ser Gly Ala Tyr Gly Tyr						
	15		20	25		
AGT AAC CCT AAG ATC CTA AAA CAG AGC ATG ACC TTG AAC CTG GCC GAC						746
Ser Asn Pro Lys Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp						
	30		35	40		
CCG GTG GGC AGT CTG AAG CCG CAC CTC CGC GCC AAG AAC TCG GAC CTT						794
Pro Val Gly Ser Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu						
	45		50	55		60
CTC ACG TCG CCC GAC GTC GGG CTG CTC AAG CTG GCG TCG CCG GAG CTG						842
Leu Thr Ser Pro Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu						
		65		70		75
GAG CGC CTG ATC ATC CAG TCC AGC AAT GGG CAC ATC ACC ACT ACA CCG						890
Glu Arg Leu Ile Ile Gln Ser Ser Asn Gly His Ile Thr Thr Pro						
		80		85		90
ACC CCC ACC CAG TTC TTG TGC CCC AAG AAC GTG ACC GAC GAG CAG GAG						938
Thr Pro Thr Gln Phe Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu						
		95		100		105
GGC TTC GCC GAG GGC TTC GTG CGC GCC CTG GCT GAA CTG CAT AGC CAG						986
Gly Phe Ala Glu Gly Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln						
	110		115		120	
AAC ACG CTT CCC AGT GTC ACC TCC GCG GCA CAG CCG GTC AGC GGG GCG						1034
Asn Thr Leu Pro Ser Val Thr Ser Ala Ala Gln Pro Val Ser Gly Ala						
	125		130		135	140
GGC ATG GTG GCT CCC GCG GTG GCC TCA GTA GCA GGC GCT GGC GGC GGT						1082
Gly Met Val Ala Pro Ala Val Ala Ser Val Ala Gly Ala Gly Gly Gly						
		145		150		155
GGT GGC TAC AGC GCC AGC CTG CAC AGT GAG CCT CCG GTC TAC GCC AAC						1130
Gly Gly Tyr Ser Ala Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn						
		160		165		170
CTC AGC AAC TTC AAC CCG GGT GCG CTG AGC AGC GGC GGT GGG GCG CCC						1178
Leu Ser Asn Phe Asn Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro						
		175		180		185
TCC TAT GGC GCG GCC GGG CTG GCC TTT CCC TCG CAG CCG CAG CAG CAG						1226
Ser Tyr Gly Ala Ala Gly Leu Ala Phe Pro Ser Gln Pro Gln Gln Gln						
	190		195		200	
CAG CAG CCG CCT CAG CCG CCG CAC CAC TTG CCC CAA CAG ATC CCG GTG						1274
Gln Gln Pro Pro Gln Pro Pro His His Leu Pro Gln Gln Ile Pro Val						
	205		210		215	220

CAG CAC CCG CGG CTG CAA GCC CTG AAG GAA GAG CCG CAG ACC GTG CCG	1322
Gln His Pro Arg Leu Gln Ala Leu Lys Glu Glu Pro Gln Thr Val Pro	
225 230 235	
GAG ATG CCG GGA GAG ACG CCG CCC CTG TCC CCT ATC GAC ATG GAG TCT	1370
Glu Met Pro Gly Glu Thr Pro Pro Leu Ser Pro Ile Asp Met Glu Ser	
240 245 250	
CAG GAG CCG ATC AAG GCA GAG AGG AAG CGC ATG AGG AAC CGC ATT GCC	1418
Gln Glu Arg Ile Lys Ala Glu Arg Lys Arg Met Arg Asn Arg Ile Ala	
255 260 265	
GCC TCC AAG TGC CGG AAA AGG AAG CTG GAG CGG ATC GCT CGG CTA GAG	1466
Ala Ser Lys Cys Arg Lys Arg Lys Leu Glu Arg Ile Ala Arg Leu Glu	
270 275 280	
GAA AAA GTG AAA ACC TTG AAA GCG CAA AAC TCC GAG CTG GCA TCC ACG	1514
Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr	
285 290 295 300	
GCC AAC ATG CTC AGG GAA CAG GTG GCA CAG CTT AAG CAG AAA GTC ATG	1562
Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys Val Met	
305 310 315	
AAC CAC GTT AAC AGT GGG TGC CAA CTC ATG CTA ACG CAG CAG TTG CAA	1610
Asn His Val Asn Ser Gly Cys Gln Leu Met Leu Thr Gln Gln Leu Gln	
320 325 330	
ACG TTT TGAGAACAGA CTGTCAGGGC TGAGGGGCAA TGGAAGAAAA AAAATAACAG	1666
Thr Phe	
AGACAAACTT GAGAACTTGA CTGGTTGCGA CAGAGAAAAA AAAAGTGTCC GAGTACTGAA	1726
GCCAAAGGGTA CACAAGATGG ACTGGGTTCC GACTGACGGC GCCCCCAGTG TGCTCTGGAG	1786
TGGGAAGGAC GTGGCGCGCC TGGCTTTGGC GTGGAGCCAG AGAGCAGGCC TATTGGCCGG	1846
CAGACTTTGC GGAGCGCTGT GCCGCGCGCG ACCAGAACGA TGGACTTTTC GTTAACATTG	1906
ACCAAGAACT GCATGGACCT AACATTTCGAT CTCATTTCAGT ATTAAAGGGG GGTGGGAGGG	1966
GTTACAAACT GCAATAGAGA CTGTAGATTG CTTCTGTAGT GCTCCTTAAC ACAAAGCAGG	2026
GAGGGCTGGG AAGGGGGGGA GGCTTGTAAG TGCCAGGCTA GACTGCAGAT GAACTCCCCT	2086
GGCCTGCCCTC TCTCAACTGT GTATGTACAT ATATATTTTT TTTTAATTTG ATGAAAGCTG	2146
ATTACTGTCA ATAAACAGCT TCCTGCCTTT GTAAGTTATT CCATGTTTGT TTGTTTGGGT	2206
GTCCTGCCCA GTGTTTGTAA ATAAGAGATT TGAAGCATTC TGAGTTTACC ATTTGTAATA	2266
AAGTATATAA TTTTTTTATG TTTTGTCTTCT GAAAATTTCC AGAAAGGATA TTTAAGAAAA	2326
TACAATAAAC TATTGAAAAG T	2347

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala	
1 5 10 15	
Ser Phe Leu Gln Ser Glu Ser Gly Ala Tyr Gly Tyr Ser Asn Pro Lys	
20 25 30	

Ile	Leu	Lys	Gln	Ser	Met	Thr	Leu	Asn	Leu	Ala	Asp	Pro	Val	Gly	Ser
		35					40					45			
Leu	Lys	Pro	His	Leu	Arg	Ala	Lys	Asn	Ser	Asp	Leu	Leu	Thr	Ser	Pro
	50					55				60					
Asp	Val	Gly	Leu	Leu	Lys	Leu	Ala	Ser	Pro	Glu	Leu	Glu	Arg	Leu	Ile
	65				70					75					80
Ile	Gln	Ser	Ser	Asn	Gly	His	Ile	Thr	Thr	Thr	Pro	Thr	Pro	Thr	Gln
				85				90						95	
Phe	Leu	Cys	Pro	Lys	Asn	Val	Thr	Asp	Glu	Gln	Glu	Gly	Phe	Ala	Glu
			100					105					110		
Gly	Phe	Val	Arg	Ala	Leu	Ala	Glu	Leu	His	Ser	Gln	Asn	Thr	Leu	Pro
		115					120					125			
Ser	Val	Thr	Ser	Ala	Ala	Gln	Pro	Val	Ser	Gly	Ala	Gly	Met	Val	Ala
	130					135					140				
Pro	Ala	Val	Ala	Ser	Val	Ala	Gly	Ala	Gly	Gly	Gly	Gly	Gly	Tyr	Ser
	145				150				155						160
Ala	Ser	Leu	His	Ser	Glu	Pro	Pro	Val	Tyr	Ala	Asn	Leu	Ser	Asn	Phe
			165					170						175	
Asn	Pro	Gly	Ala	Leu	Ser	Ser	Gly	Gly	Gly	Ala	Pro	Ser	Tyr	Gly	Ala
			180				185						190		
Ala	Gly	Leu	Ala	Phe	Pro	Ser	Gln	Pro	Gln	Gln	Gln	Gln	Gln	Pro	Pro
	195						200					205			
Gln	Pro	Pro	His	His	Leu	Pro	Gln	Gln	Ile	Pro	Val	Gln	His	Pro	Arg
	210				215						220				
Leu	Gln	Ala	Leu	Lys	Glu	Glu	Pro	Gln	Thr	Val	Pro	Glu	Met	Pro	Gly
	225				230					235					240
Glu	Thr	Pro	Pro	Leu	Ser	Pro	Ile	Asp	Met	Glu	Ser	Gln	Glu	Arg	Ile
			245					250						255	
Lys	Ala	Glu	Arg	Lys	Arg	Met	Arg	Asn	Arg	Ile	Ala	Ala	Ser	Lys	Cys
			260					265					270		
Arg	Lys	Arg	Lys	Leu	Glu	Arg	Ile	Ala	Arg	Leu	Glu	Glu	Lys	Val	Lys
		275					280					285			
Thr	Leu	Lys	Ala	Gln	Asn	Ser	Glu	Leu	Ala	Ser	Thr	Ala	Asn	Met	Leu
	290				295						300				
Arg	Glu	Gln	Val	Ala	Gln	Leu	Lys	Gln	Lys	Val	Met	Asn	His	Val	Asn
	305				310					315					320
Ser	Gly	Cys	Gln	Leu	Met	Leu	Thr	Gln	Gln	Leu	Gln	Thr	Phe		
			325					330							

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATACCAGAGA	CTCAAAAAA	AAAAAAAGT	TCCAGATTGC	TGGACAATGA	CCCGGGTCTC	60
ATCCCTTGAC	CCTGGGAACC	GGGTCCACAT	TGAATCAGGT	GCGAATGTTT	GCTCGCCTTC	120
TCTGCCTTTT	CCGCCTCCCC	TCCCCCGGCC	GCGGCCCGG	TTCCCCCCT	GCGCTGCACC	180
CTCAGAGTTG	GCTGCAGCCG	GCGAGCTGTT	CCCGTCAATC	CCTCCCTCCT	TTACACAGGA	240
TGTCCATATT	AGGACATCTG	CGTCAGCAGG	TTTCCACGGC	CGGTCCCTGT	TGTTCTGGGG	300
GGGGGACCAT	CTCCGAAATC	CTACACGCGG	AAGGTCTAGG	AGACCCCTA	AGATCCCAAA	360
TGTGAACACT	CATAGGTGAA	AGATGTATGC	CAAGACGGGG	GTTGAAAGCC	TGGGGCGTAG	420
AGTTGACGAC	AGAGCGCCCG	CAGAGGGCCT	TGGGGCGCGC	TTCCCCCCCC	TTCCAGTTCC	480
GCCCAGTGAC	GTAGGAAGTC	CATCCATTCA	CAGCGCTTCT	ATAAAGGCGC	CAGCTGAGGC	540
GCCTACTACT	CCAACCGCGA	CTGCAGCGAG	CAACTGAGAA	GACTGGATAG	AGCCGGCGGT	600

TCCGCGAACG	AGCAGTGACC	GCGCTCCCAC	CCAGCTCTGC	TCTGCAGCTC	CCACCAGTGT	660
CTACCCCTGG	ACCCCTTGCC	GGGCTTTCCC	CAAACCTCGA	CCATGATGTT	CTCGGGTTTC	720
AACGCCGACT	ACGAGGCGTC	ATCCTCCCAG	TGCAGTAGCG	CCTCCCCGGC	CGGGGACAGC	780
CTTTCTACT	ACCATTTCCC	AGCCGACTCC	TTCTCCAGCA	TGGGCTCTCC	TGTCAACACA	840
CAGGTGAGTT	TGGCTTTGTG	TAGCCGCCAG	GTCCGCGCTG	AGGGTCGCCG	TGGAGGAGAC	900
ACTGGGGTGT	GACTCGCAGG	GGCGGGGGGG	TCTTCCTTTT	TCGCTCTGGA	GGGAGACTGG	960
CGCGGTCAGA	GCAGCCTTAG	CCTGGGAACC	CAGGACTTGT	CTGAGCGCGT	GCACACTTGT	1020
CATAGTAAGA	CTTAGTGACC	CCTTCCCAGC	CGGCAGGTTT	ATTCTGAGTG	GCCTGCCTGC	1080
ATTCTTCTCT	CGGCCGACTT	GTTTCTGAGA	TCAGCCGGGG	CCAACAAGTC	TCGAGCAAAG	1140
AGTCGCTAAC	TAGAGTTTGG	GAGGCGGCAA	ACCGCGGCAA	TCCCCCTCC	CGGGGCAGCC	1200
TGGAGCAGGG	AGGAGGGAGG	AGGGAGGAGG	GTGCTGCGGG	CGGGTGTGTA	AGGCAGTTTC	1260
ATTGATAAAA	AGCGAGTTCA	TTCTGGAGAC	TCCGGAGCAG	CGCCTGCGTC	AGCGCAGACG	1320
TCAGGGATAT	TTATAACAAA	CCCCCTTTTC	AGCGAGTGAT	GCCGAAGGGA	TAACGGGAAC	1380
GCAGCAGTAG	GATGGAGGAG	AAAGGCTGCG	CTGCGGAATT	CAAGGGAGGA	TATTGGGAGA	1440
GCTTTTATCT	CCGATGAGGT	GCATACAGGA	AGACATAAGC	AGTCTCTGAC	CGGAATGCTT	1500
CTCTCTCCCT	GCTTCATGCG	ACACTAGGGC	CATTGTCTCC	ACCTGTGTCT	GGAACCTCCT	1560
CGCTCACCTC	CGCTTTCTCT	TTTTTGTTTT	GTTTCAGGAC	TTTTGCGCAG	ATCTGTCCGT	1620
CTCTAGTGCC	AACTTTATCC	CCACGGTGAC	AGCCATCTCC	ACCAGCCCAG	ACCTGCAGTG	1680
GCTGGTGCAG	CCCACTCTGG	TCTCCTCCGT	GGCCCCATCG	CAGACCAGAG	CGCCCCATCC	1740
TTACGGACTC	CCCACCCAGT	CTGCTGGGGC	TTACGCCAGA	GCGGGAATGG	TGAAGACCGT	1800
GTCAGGAGGC	AGAGCGCAGA	GCATCGGCAG	AAGGGGCAAA	GTAGAGCAGG	TGAGCAGCGA	1860
TTCTGGACCT	TTGTGGGCTG	GGGGGGGGGG	GGGGGGCGGA	GACTGACGCA	CAGACCACAC	1920
AACAGAGAAG	GGACGCTACT	GACTGCACTT	CCTGACCAGG	AGCTGTGGCT	GCTAGCCCTT	1980
TCCCTCCCTT	GTCAGATTTT	GACAGTTGGA	CCCAAGACAA	ACTCTAGACA	GTTTCCCTGA	2040
CAGCTTCCTA	CTTCATTCTC	TAGCCGGGGA	GCTTCTTTGT	TCCCCTGCTA	AAGATCTCAC	2100
TTTAAATGCA	AATCACACTC	TGCCTGCCAA	CTGCAGGTTA	GAAAACTGCT	TTCACCGAGA	2160
GGTGCGGGTG	CTGTAGGAGC	CAGTTTCACT	GGGGTGAAGT	AATGGAGGTG	ACACTAGACA	2220
ACCTTAACTG	AATGTTGGTC	CTTTTCTTCT	ATAGCTATCT	CCTGAAGAGG	AAGAGAAACG	2280
GAGAATCCGA	AGGGAACGGA	ATAAGATGGC	TGCAGCCAA	TGCCGGAATC	GGAGGAGGGA	2340
GCTGACAGAT	ACACTCCAAG	CGGTAGGTTG	AACCAGCTGC	TGCTCCTGAA	ACTTTATTAA	2400
AGTTGGAGCT	TGGGACTATG	GGCGCAGGGT	CCTTGAGCAT	GCCCGTGTCT	TATGCTTTCT	2460
TATATCTCTC	CCTATGCAGG	AGACAGATCA	ACTTGAAGAT	GAGAAGTCTG	CGTTGCAGAC	2520
TGAGATTGCC	AATCTGCTGA	AAGAGAAGGA	AAAACCTGGG	TTTATTTTGG	CAGCCCACCG	2580
ACCTGCCTGC	AAGATCCCCG	ATGACCTTGG	CTTCCCAGAG	GAGATGTCTG	TGGCCTCCCT	2640
GGATTGACT	GGAGGTCTGC	CTGAGGCTTC	CACCCCAGAG	TCTGAGGAGG	CCTTCACCCT	2700
GCCCCCTTCT	AACGACCCTG	AGCCCAAGCC	ATCCTTGAGG	CCAGTCAAGA	GCATCAGCAA	2760
CGTGGAGCTG	AAGGCAGAAC	CCTTTGATGA	CTTCTTGTTT	CCGGCATCAT	CTAGGCCAG	2820
TGGCTCAGAG	ACCTCCCCTG	CTGTGCCAGA	TGTGGACCTG	TCCGGTTCCT	TCTATGCAGC	2880
AGACTGGGAG	CCTCTGCACA	GCAATTCCTT	GGGGATGGGG	CCCATGGTCA	CAGAGCTGGA	2940
GCCCCCTGTGT	ACTCCCCTGG	TCACCTGTAC	TCCGGGCTGC	ACTACTTACA	CGTCTTCCTT	3000
TGTCTTCACC	TACCCTGAAG	CTGACTCCTT	CCCAAGCTGT	GCCGCTGCCC	ACCGAAAGGG	3060
CAGCAGCAGC	AACGAGCCCT	CCTCCGACTC	CCTGAGCTCA	CCCACGCTGC	TGGCCCTGTG	3120
AGCAGTCAGA	GAAGGCAAGG	CAGCCGGCAT	CCAGACGTGC	CACTGCCCCG	GCTGGTGCAT	3180
TACAGAGAGG	AGAAACACGT	CTTCCCTCGA	AGGTTCCCGT	CGACCTAGGG	AGGACCTTAC	3240
CTGTTCTGTA	AACACACCAG	GCTGTGGGCC	TCAAGGACTT	GCAAGCATCC	ACATCTGGCC	3300
TCCAGTCCTC	ACCTCTTCCA	GAGATGTAGC	AAAAACAAAA	CAAAACAAAA	CAAAAAACCG	3360
CATGGAGTGT	GTGTTTCCTA	GTGACACCTG	AGAGCTGGTA	GTTAGTAGAG	CATGTGAGTC	3420
AAGGCCTGGT	CTGTGTCTCT	TTTCTCTTTC	TCCTTAGTTT	TCTCATAGCA	CTAACTAATC	3480
TGTTGGGTTT	ATTATTGGAA	TTAACCTGGT	GCTGGATTGT	ATCTAGTGCA	GCTGATTTTA	3540
ACAATACCTA	CTGTGTTCCCT	GGCAATAGCG	TGTTCCCAAT	AGAAACGACC	AATATTAAAC	3600
TAAGAAAAGA	TAGGACTTTA	TTTTCCAGTA	GATAGAAATC	AATAGCTATA	TCCATGTACT	3660
GTAGTCCTTC	AGCGTCAATG	TTCATTGTCA	TGTTACTGAT	CATGCATTGT	CGAGGTGGTC	3720
TGAATGTTCT	GACATTAACA	GTTTTCCATG	AAAACGTTTT	TATTGTGTTT	TCAATTTATT	3780
TATTAAGATG	GATTCTCAGA	TATTTATATT	TTTTTTTAT	TTTTTTCTAC	CCTGAGGTCT	3840
TTTCGACATG	GGAAAGTGAA	TTTGAATGAA	AAATTTTAAG	CATTGTTTGC	TTATTGTTCC	3900
AGGACATTGT	CAATAAAAGC	ATTTAAGTTG	AATGCGACCA	CCTTCTTGCT	CTCTTTATTC	3960
TCAGTTT						3967

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Met	Phe	Ser	Gly	Phe	Asn	Ala	Asp	Tyr	Glu	Ala	Ser	Ser	Ser	Arg
1				5					10					15	
Cys	Ser	Ser	Ala	Ser	Pro	Ala	Gly	Asp	Ser	Leu	Ser	Tyr	Tyr	His	Ser
			20					25					30		
Pro	Ala	Asp	Ser	Phe	Ser	Ser	Met	Gly	Ser	Pro	Val	Asn	Thr	Gln	Asp
		35					40					45			
Phe	Cys	Ala	Asp	Leu	Ser	Val	Ser	Ser	Ala	Asn	Phe	Ile	Pro	Thr	Val
	50					55				60					
Thr	Ala	Ile	Ser	Thr	Ser	Pro	Asp	Leu	Gln	Trp	Leu	Val	Gln	Pro	Thr
	65				70				75					80	
Leu	Val	Ser	Ser	Val	Ala	Pro	Ser	Gln	Thr	Arg	Ala	Pro	His	Pro	Tyr
			85					90					95		
Gly	Leu	Pro	Thr	Gln	Ser	Ala	Gly	Ala	Tyr	Ala	Arg	Ala	Gly	Met	Val
			100				105						110		
Lys	Thr	Val	Ser	Gly	Gly	Arg	Ala	Gln	Ser	Ile	Gly	Arg	Arg	Gly	Lys
	115					120					125				
Val	Glu	Gln	Leu	Ser	Pro	Glu	Glu	Glu	Lys	Arg	Arg	Ile	Arg	Arg	
	130					135				140					
Glu	Arg	Asn	Lys	Met	Ala	Ala	Ala	Lys	Cys	Arg	Asn	Arg	Arg	Arg	Glu
	145				150					155					160
Leu	Thr	Asp	Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys
			165					170					175		
Ser	Ala	Leu	Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys
		180						185				190			
Leu	Glu	Phe	Ile	Leu	Ala	Ala	His	Arg	Pro	Ala	Cys	Lys	Ile	Pro	Asp
	195						200					205			
Asp	Leu	Gly	Phe	Pro	Glu	Glu	Met	Ser	Val	Ala	Ser	Leu	Asp	Leu	Thr
	210					215					220				
Gly	Gly	Leu	Pro	Glu	Ala	Ser	Thr	Pro	Glu	Ser	Glu	Glu	Ala	Phe	Thr
	225				230					235				240	
Leu	Pro	Leu	Leu	Asn	Asp	Pro	Glu	Pro	Lys	Pro	Ser	Leu	Glu	Pro	Val
			245						250					255	
Lys	Ser	Ile	Ser	Asn	Val	Glu	Leu	Lys	Ala	Glu	Pro	Phe	Asp	Asp	Phe
		260						265				270			
Leu	Phe	Pro	Ala	Ser	Ser	Arg	Pro	Ser	Gly	Ser	Glu	Thr	Ser	Arg	Ser
	275					280						285			
Val	Pro	Asp	Val	Asp	Leu	Ser	Gly	Ser	Phe	Tyr	Ala	Ala	Asp	Trp	Glu
	290					295					300				
Pro	Leu	His	Ser	Asn	Ser	Leu	Gly	Met	Gly	Pro	Met	Val	Thr	Glu	Leu
	305				310					315				320	
Glu	Pro	Leu	Cys	Thr	Pro	Val	Val	Thr	Cys	Thr	Pro	Gly	Cys	Thr	Thr
			325						330					335	
Tyr	Thr	Ser	Ser	Phe	Val	Phe	Thr	Tyr	Pro	Glu	Ala	Asp	Ser	Phe	Pro
		340					345						350		
Ser	Cys	Ala	Ala	Ala	His	Arg	Lys	Gly	Ser	Ser	Ser	Asn	Glu	Pro	Ser
		355					360					365			
Ser	Asp	Ser	Leu	Ser	Ser	Pro	Thr	Leu	Leu	Ala	Leu				
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGAAATGGA GGCTCATAAA TACCACAGCT

30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATTGGAAGAA GACCAAAGCA AGAGCAACTA

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAAGTAAGTA GTGCTGTATG AATACAGACA

30

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TACTGGCAAT ATATTACAGA TGGGTTTATG

30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGTGCAGCT TATGATGCTA TTCTTGAA 28

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGCGTCACCA CATACGGAGT CATC 24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGGAGGAGT TCCAAGATGT CTACT 25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGAAAGAGC TTGGGGAAGG TGAG 24